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| APPLICATION NO. | FILING DATE | FIRST NAMED INVENTOR | ATTORNEY DOCKET NO. | CONFIRMATION NO. |
|-----------------|-------------|----------------------|---------------------|------------------|
| 09/831,452      | 06/10/2001  | Kazuo Sugamura       | 2001-0572A          | 4276             |

513 7590 03/02/2007  
WENDEROTH, LIND & PONACK, L.L.P.  
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SUITE 800  
WASHINGTON, DC 20006-1021

|          |
|----------|
| EXAMINER |
|----------|

BASI, NIRMAL SINGH

|          |              |
|----------|--------------|
| ART UNIT | PAPER NUMBER |
|----------|--------------|

1646

| SHORTENED STATUTORY PERIOD OF RESPONSE | MAIL DATE  | DELIVERY MODE |
|--|------------|---------------|
| 3 MONTHS                               | 03/02/2007 | PAPER         |

**Please find below and/or attached an Office communication concerning this application or proceeding.**

If NO period for reply is specified above, the maximum statutory period will apply and will expire 6 MONTHS from the mailing date of this communication.

**Office Action Summary**

Application No.

09/831,452

Applicant(s)

SUGAMURA ET AL.

Examiner

Nirmal S. Basi

Art Unit

1646

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

**Period for Reply**

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

**Status**

- 1) ☒ Responsive to communication(s) filed on 22 August 2006.
- 2a) ☐ This action is **FINAL**. 2b) ☒ This action is non-final.
- 3) ☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

**Disposition of Claims**

- 4) ☒ Claim(s) 1-3 and 5 is/are pending in the application.
- 4a) Of the above claim(s) \_\_\_\_\_ is/are withdrawn from consideration.
- 5) ☐ Claim(s) \_\_\_\_\_ is/are allowed.
- 6) ☒ Claim(s) 1, 2, 3 and 5 is/are rejected.
- 7) ☐ Claim(s) \_\_\_\_\_ is/are objected to.
- 8) ☐ Claim(s) \_\_\_\_\_ are subject to restriction and/or election requirement.

**Application Papers**

- 9) ☐ The specification is objected to by the Examiner.
- 10) ☐ The drawing(s) filed on \_\_\_\_\_ is/are: a) ☐ accepted or b) ☐ objected to by the Examiner.  
Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).  
Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).
- 11) ☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

**Priority under 35 U.S.C. § 119**

- 12) ☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).
- a) ☐ All b) ☐ Some \* c) ☐ None of:
- ☐ Certified copies of the priority documents have been received.
  - ☐ Certified copies of the priority documents have been received in Application No. \_\_\_\_\_.
  - ☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

\* See the attached detailed Office action for a list of the certified copies not received.

**Attachment(s)**

- |  |   |
|--|---|
| 1) <input checked="" type="checkbox"/> Notice of References Cited (PTO-892)          | 4) <input type="checkbox"/> Interview Summary (PTO-413)           |
| 2) <input type="checkbox"/> Notice of Draftsperson's Patent Drawing Review (PTO-948) | Paper No(s)/Mail Date. _____                                      |
| 3) <input type="checkbox"/> Information Disclosure Statement(s) (PTO/SB/08)          | 5) <input type="checkbox"/> Notice of Informal Patent Application |
| Paper No(s)/Mail Date _____  | 6) <input type="checkbox"/> Other: _____                          |

### **DETAILED ACTION**

1. Applicant's request for reconsideration of the finality of the rejection of the last Office action is persuasive and, therefore, the finality of that action is withdrawn.
2. Prosecution on the merits of this application is reopened on claims 1-3 and 5 considered unpatentable for the reasons indicated below:

#### ***Response to Amendment***

3. Applicant's arguments filed 8/22/06, with respect to the rejection(s) of claim(s) 2 and 3 under 35 USC § 102 and claim 5 under 35 USC § 102 have been fully considered. The rejections have been recast to better address Applicant's arguments. It is noted that the previous examiner did not address claim 1 in the final rejection, this claim is also addressed below. The rejections below can be considered as new grounds of rejection.

#### ***Claim Rejections - 35 USC § 103***

4. The following is a quotation of 35 U.S.C. 103(a) which forms the basis for all obviousness rejections set forth in this Office action:

(a) A patent may not be obtained though the invention is not identically disclosed or described as set forth in section 102 of this title, if the differences between the subject matter sought to be patented and the prior art are such that the subject matter as a whole would have been obvious at the time the invention was made to a person having ordinary skill in the art to which said subject matter pertains. Patentability shall not be negated by the manner in which the invention was made.

The factual inquiries set forth in *Graham v. John Deere Co.*, 383 U.S. 1, 148 USPQ 459 (1966), that are applied for establishing a background for determining obviousness under 35 U.S.C. 103(a) are summarized as follows:

Art Unit: 1646

1. Determining the scope and contents of the prior art.
2. Ascertaining the differences between the prior art and the claims at issue.
3. Resolving the level of ordinary skill in the pertinent art.
4. Considering objective evidence present in the application indicating obviousness or nonobviousness.

This application currently names joint inventors. In considering patentability of the claims under 35 U.S.C. 103(a), the examiner presumes that the subject matter of the various claims was commonly owned at the time any inventions covered therein were made absent any evidence to the contrary. Applicant is advised of the obligation under 37 CFR 1.56 to point out the inventor and invention dates of each claim that was not commonly owned at the time a later invention was made in order for the examiner to consider the applicability of 35 U.S.C. 103(c) and potential 35 U.S.C. 102(e), (f) or (g) prior art under 35 U.S.C. 103(a).

Claims 1, 3 and 5 are rejected under 35 U.S.C. 103(a) as being unpatentable over Yu *et al* (1997, *Genome Res.* 7(4): 353-358) in view of Hutchinson *et al* (Nucleic Acids Research, 1992, Vol. 20, No.13, pages 345-3462) and further in view of Solovyev *et al* (Nucleic Acids Research, 1994, Vol. 22, No.24, pages 5156-5163) and Eberhard Passarge (Color Atlas of Genetics, Georg Thieme Verlag Stuttgart, New York, Thieme Medical publishers, Inc. New York, 1995).

Yu *et al.* teach a polynucleotide that is 100% identical to SEQ ID NO: 2 of the current application over a span of 1356 base pairs (see GenBank Accession No. AF052135 (submitted March 5, 1998) and attached alignment-spanning bp 1-1356 of SEQ ID NO: 2). The polynucleotide was contained in a vector. The polynucleotide sequence of Yu *et al.* contains the polynucleotide of SEQ ID NO:2, which encodes the

Art Unit: 1646

polypeptide of SEQ ID NO:1. Yu *et al.* does not disclose the polypeptide of SEQ ID NO:2, nor does it disclose which specific fragment of the polynucleotide encodes the polypeptide. Yu (AF052135) does not specifically disclose the start or stop coding regions for the protein but it is apparent from the sequence, based on the teaching in the art (some of which are given below) that Yu (AF052135) contains three candidates for the start codons (117-119; 127-129; 133-135) and one stop codon (1481-1483).

Therefore, one of skill in the art can ascertain that since there are three start sites and one stop codon then three polypeptides can be translated using the polynucleotide of SEQ ID NO:2. Yu *et al.* does not specifically point out the start and stop codons or method of their use in predicting structure but the level of skill was high in the Molecular Biology arts at the time of filing instant application that this type of analysis was routine, for example:

Hutchinson discloses the state of the art in molecular Biology, where as far back as 1992 computer programs were available that identified coding sequences in long stretches of DNA and predicted translation product of these DNA sequences into their amino acid residues. These sequences were translated to identify and purify new proteins as well as provide databases for searching homologous proteins.

Solovyev discloses the state of the art in molecular Biology, where as far back as 1994 computer programs were available that identified coding sequences in long stretches of DNA and translation of these DNA sequences into their amino acid residues. These sequences were translated to identify and purify new proteins as well

Eberhard Passarge discloses that significance of codon usage as it applies to its encoded polypeptides was well known in the art at the time of filing instant application.

The sequence alignments of AF052135 are given below.

## ALIGNMENTS

## Protein alignment to DNA

AF052135

|             |          |         |      |        |     |
|-------------|----------|---------|------|--------|-----|
| LOCUS       | AF052135 | 1462 bp | mRNA | linear | PRI |
| 05-AUG-1998 |          |         |      |        |     |

DEFINITION Homo sapiens clone 23625 mRNA sequence.

ACCESSION AF052135

VERSION AF052135.1 GI:3360444

KEYWORDS FLI CDNA.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1462)

AUTHORS    Andersson, B., Wentland, M.A., Ricafrente, J.Y., Liu, W. and

Gibbs, R.A.

TITLE A 'double adaptor' method for improved shotgun library  
construction

JOURNAL Anal. Biochem. 236 (1), 107-113 (1996)

MEDLINE 96207227

PUBMED 8619474

REFERENCE 2 (bases 1 to 1462)

**AUTHORS** Yu, W., Andersson, B., Worley, K.C., Muzny, D.M., Ding, Y., Liu, W., Ricafrente, J.Y., Wentland, M.A., Lennon, G. and Gibbs, R.A.

TITLE Large-scale concatenation cDNA sequencing

JOURNAL      **Genome Res. 7 (4), 353-358 (1997)**

MEDLINE 97264341

PUBMED 9110174

REFERENCE 3 (bases 1 to 1462)

AUTHORS Yu, W., Sarginson, J. and Gibbs, R.A.

TITLE Direct Submission

JOURNAL Submitted (05-MAR-1998) Molecular and Human Genetics, Baylor

College of Medicine, One Baylor Plaza S930, Houston, TX 77030, USA

| FEATURES | Location/Qualifiers |
|----------|---------------------|
|----------|---------------------|

Art Unit: 1646

source 1. .1462  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="I.M.A.G.E. Consortium clone ID 23625"  
/sex="female"  
/tissue\_type="brain"  
/clone\_lib="1NIB"  
/dev\_stage="infant"

## ORIGIN

## Alignment Scores:

|                        |           |               |      |
|------------------------|-----------|---------------|------|
| Pred. No.:             | 3.57e-171 | Length:       | 1462 |
| Score:                 | 2208.00   | Matches:      | 424  |
| Percent Similarity:    | 100.00%   | Conservative: | 0    |
| Best Local Similarity: | 100.00%   | Mismatches:   | 0    |
| Query Match:           | 100.00%   | Indels:       | 0    |
| DB:                    | 9         | Gaps:         | 0    |

US-09-831-452-1 (1-424) x AF052135 (1-1462)

|    |     |   |     |
|----|-----|---|-----|
| Qy | 1   | MetSerAspHisGlyAspValSerLeuProProGluAspArgValArgAlaLeuSerGln  | 20  |
| Db | 117 | ATGTCTGACCATGGAGATGTGAGCCTCCCGCCCGAAGACCGGGTGAGGGCTCTCTCCAG   | 176 |
| Qy | 21  | LeuGlySerAlaValGluValAsnGluAspIleProProArgArgTyrPheArgSerGly  | 40  |
| Db | 177 | CTGGGTAGTGCGGTAGAGGTGAATGAAGACATTCCACCCCGTCGGTACTTCCGCTCTGGA  | 236 |
| Qy | 41  | ValGluIleIleArgMetAlaSerIleTyrSerGluGluGlyAsnIleGluHisAlaPhe  | 60  |
| Db | 237 | GTTGAGATTATCCGAATGGCATCCATTTACTCTGAGGAAGGCAACATTGAACATGCCTTC  | 296 |
| Qy | 61  | IleLeuTyrAsnLysTyrIleThrLeuPheIleGluLysLeuProLysHisArgAspTyr  | 80  |
| Db | 297 | ATCCTCTATAACAAGTATATACGCTCTTTATTGAGAACTACCAAACATCGAGATTAC     | 356 |
| Qy | 81  | LysSerAlaValIleProGluLysLysAspThrValLysLysLeuLysGluIleAlaPhe  | 100 |
| Db | 357 | AAATCTGCTGTTCATTCCTGAAAAGAAAGACACAGTAAAGAAATTAAAGGAGATTGCATTT | 416 |
| Qy | 101 | ProLysAlaGluGluLeuLysAlaGluLeuLeuLysArgTyrThrLysGluTyrThrGlu  | 120 |
| Db | 417 | CCCAAAGCAGAAGAGCTGAAGGCAGAGCTGTAAAACGATATACCAAAGAATATACAGAA   | 476 |
| Qy | 121 | TyrAsnGluGluLysLysLysGluAlaGluGluLeuAlaArgAsnMetAlaIleGlnGln  | 140 |
| Db | 477 | TATAATGAAGAAAAGAAGAAGGAAGCAGAGGAATTGGCCCGGAACATGGCCATCCAGCAA  | 536 |
| Qy | 141 | GluLeuGluLysGluLysGlnArgValAlaGlnGlnLysGlnGlnGlnLeuGluGlnGlu  | 160 |
| Db | 537 | GAGCTGGAAGAAAGAAAACAGAGGGTAGCACAACAGAAGCAGCAGCAATTGGAACAGGAA  | 596 |
| Qy | 161 | GlnPheHisAlaPheGluGluMetIleArgAsnGlnGluLeuGluLysGluArgLeuLys  | 180 |

Art Unit: 1646

Db 597 CAGTTCCATGCCTTCGAGGAGATGATCCGGAACCAGGAGCTAGAAAAAGAGCGACTGAAA 656  
Qy 181 IleValGlnGluPheGlyLysValAspProGlyLeuGlyGlyProLeuValProAspLeu 200  
Db 657 ATTGTACAGGAGTTTGGGAAGGTAGACCCTGGCCTAGGTGGCCCGCTAGTGCCTGACTTG 716  
Qy 201 GluLysProSerLeuAspValPheProThrLeuThrValSerSerIleGlnProSerAsp 220  
Db 717 GAGAAGCCCTCCTTAGATGTGTTCCCCACCTTAACAGTCTCATCCATACAGCCTTCAGAC 776  
Qy 221 CysHisThrThrValArgProAlaLysProProValValAspArgSerLeuLysProGly 240  
Db 777 TGTCAACAACCTGTAAGGCCAGCTAAGCCACCTGTGGTGGACAGGTCCTTGAAACCTGGA 836  
Qy 241 AlaLeuSerAsnSerGluSerIleProThrIleAspGlyLeuArgHisValValValPro 260  
Db 837 GCACTGAGCAACTCAGAAAGTATTCCCACAATCGATGGATTGCGCCATGTGGTGGTGCT 896  
Qy 261 GlyArgLeuCysProGlnPheLeuGlnLeuAlaSerAlaAsnThrAlaArgGlyValGlu 280  
Db 897 GGGCGGCTGTGCCCACAGTTTCTCCAGTTAGCCAGTGCCAACACTGCCCCGGGAGTGGAG 956  
Qy 281 ThrCysGlyIleLeuCysGlyLysLeuMetArgAsnGluPheThrIleThrHisValLeu 300  
Db 957 ACATGTGGAATTCTCTGTGGAAACTGATGAGGAATGAATTTACCATTACCCATGTTCTC 1016  
Qy 301 IleProLysGlnSerAlaGlySerAspTyrCysAsnThrGluAsnGluGluGluLeuPhe 320  
Db 1017 ATCCCCAAGCAAAGTGCTGGGTCTGATTACTGCAACACAGAGAACGAAGAAGAACTTTTC 1076  
Qy 321 LeuIleGlnAspGlnGlnGlyLeuIleThrLeuGlyTrpIleHisThrHisProThrGln 340  
Db 1077 CTCATACAGGATCAGCAGGGCCTCATCACACTGGGCTGGATTCACTACCCCCACAG 1136  
Qy 341 ThrAlaPheLeuSerSerValAspLeuHisThrHisCysSerTyrGlnMetMetLeuPro 360  
Db 1137 ACCGCGTTTCTCTCCAGTGTGACCTACACACTCACTGCTCTTACCAGATGATGTTGCCA 1196  
Qy 361 GluSerValAlaIleValCysSerProLysPheGlnGluThrGlyPhePheLysLeuThr 380  
Db 1197 GAGTCAGTAGCCATTGTTTGCTCCCCCAAGTTCCAGGAAACTGGATTCTTTAAACTAACT 1256  
Qy 381 AspHisGlyLeuGluGluIleSerSerCysArgGlnLysGlyPheHisProHisSerLys 400  
Db 1257 GACCATGGACTAGAGGAGATTTCTTCTGTGCGCCAGAAAGGATTTCATCCACACAGCAAG 1316  
Qy 401 AspProProLeuPheCysSerCysSerHisValThrValValAspArgAlaValThrIle 420



Art Unit: 1646

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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1317 GATCCACCTCTGTTCTGTAGCTGCAGCCACGTGACTGTTGTGGACAGAGCAGTGACCATC
1376
Qy      421 ThrAspLeuArg 424
          ||||||||||||
Db      1377 ACAGACCTTCGA 1388

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Alignment DNA to DNA

## RESULT 5

AF052135

LOCUS AF052135 1462 bp mRNA linear PRI 05-AUG-1998

DEFINITION Homo sapiens clone 23625 mRNA sequence.

ACCESSION AF052135

VERSION AF052135.1 GI:3360444

KEYWORDS FLI\_CDNA.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1462)

AUTHORS Andersson,B., Wentland,M.A., Ricafrente,J.Y., Liu,W. and  
Gibbs,R.A.

TITLE A 'double adaptor' method for improved shotgun library  
construction

JOURNAL Anal. Biochem. 236 (1), 107-113 (1996)

MEDLINE 96207227

PUBMED 8619474

REFERENCE 2 (bases 1 to 1462)

AUTHORS Yu,W., Andersson,B., Worley,K.C., Muzny,D.M., Ding,Y., Liu,W.,  
Ricafrente,J.Y., Wentland,M.A., Lennon,G. and Gibbs,R.A.

TITLE Large-scale concatenation cDNA sequencing

JOURNAL Genome Res. 7 (4), 353-358 (1997)

MEDLINE 97264341

PUBMED 9110174

REFERENCE 3 (bases 1 to 1462)

AUTHORS Yu,W., Sarginson,J. and Gibbs,R.A.

TITLE Direct Submission

JOURNAL Submitted (05-MAR-1998) Molecular and Human Genetics, Baylor  
College of Medicine, One Baylor Plaza S930, Houston, TX 77030, USA

FEATURES Location/Qualifiers

source

1. .1462

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="I.M.A.G.E. Consortium clone ID 23625"

Art Unit: 1646

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## ORIGIN

Query Match 71.0%; Score 1356; DB 9; Length 1462;  
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Matches 1356; Conservative 0; Mismatches 0; Indels 0; Gaps  
0;

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        |||  
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        |||  
Qy     61 TCTCTCCAGCTGGGTTAGTGCGGTAGAGGTGAATGAAGACATTCCACCCCGTCGGTACTT 120  
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        |||  
Qy     121 CCGCTCTGGAGTTGAGATTATCCGAATGGCATCCATTTACTCTGAGGAAGGCAACATTGA 180  
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Db     227 CCGCTCTGGAGTTGAGATTATCCGAATGGCATCCATTTACTCTGAGGAAGGCAACATTGA 286  
        |||  
Qy     181 ACATGCCTTCATCCTCTATAACAAGTATATCACGCTCTTTATTGAGAACTACCAAAACA 240  
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Qy     241 TCGAGATTACAAATCTGCTGTCATTCTCTGAAAAAGAAAGACACAGTAAAGAAATTAAAGGA 300  
        |||  
Db     347 TCGAGATTACAAATCTGCTGTCATTCTCTGAAAAAGAAAGACACAGTAAAGAAATTAAAGGA 406  
        |||  
Qy     301 GATTGCATTTCCCAAAGCAGAAGAGCTGAAGGCAGAGCTGTTAAACGATATACCAAAGA 360  
        |||  
Db     407 GATTGCATTTCCCAAAGCAGAAGAGCTGAAGGCAGAGCTGTTAAACGATATACCAAAGA 466  
        |||  
Qy     361 ATATACAGAAATATAATGAAGAAAAAGAAAGGAAGCAGAGGAATTGGCCCCGGAACATGGC 420  
        |||  
Db     467 ATATACAGAAATATAATGAAGAAAAAGAAAGGAAGCAGAGGAATTGGCCCCGGAACATGGC 526  
        |||  
Qy     421 CATCCAGCAAGAGCTGGAAAAAGAAAAACAGAGGGTAGCACAAACAGAAGCAGCAGCAATT 480  
        |||  
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Qy     481 GGAACAGGAACAGTTCCATGCCTTCGAGGAGATGATCCGGAACCAGGAGCTAGAAAAAGA 540  
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Qy     541 GCGACTGAAAATTGTACAGGAGTTTGGGAAGGTAGACCCTGGCCTAGGTGGCCCGCTAGT 600  
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Qy     601 GCCTGACTTGGAGAAGCCCTCCTTAGATGTGTTCCCCACCTTAACAGTCTCATCCATACA 660  
        |||  
Db     707 GCCTGACTTGGAGAAGCCCTCCTTAGATGTGTTCCCCACCTTAACAGTCTCATCCATACA 766  
        |||
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|    |      |  |      |
|----|------|--|------|
| Qy | 661  | GCCTTCAGACTGTGCACACAACCTGTAAGGCCAGCTAAGCCACCTGTGGTGGACAGGTCCTT | 720  |
| Db | 767  | GCCTTCAGACTGTGCACACAACCTGTAAGGCCAGCTAAGCCACCTGTGGTGGACAGGTCCTT | 826  |
| Qy | 721  | GAAACCTGGAGCACTGAGCAACTCAGAAAGTATTCCCACAATCGATGGATTGCGCCATGT   | 780  |
| Db | 827  | GAAACCTGGAGCACTGAGCAACTCAGAAAGTATTCCCACAATCGATGGATTGCGCCATGT   | 886  |
| Qy | 781  | GGTGGTGCCTGGGCGGCTGTGCCCACAGTTTCTCCAGTTAGCCAGTGCCAACACTGCCCCG  | 840  |
| Db | 887  | GGTGGTGCCTGGGCGGCTGTGCCCACAGTTTCTCCAGTTAGCCAGTGCCAACACTGCCCCG  | 946  |
| Qy | 841  | GGGAGTGGAGACATGTGGAATTCTCTGTGGAAACTGATGAGGAATGAATTTACCATTAC    | 900  |
| Db | 947  | GGGAGTGGAGACATGTGGAATTCTCTGTGGAAACTGATGAGGAATGAATTTACCATTAC    | 1006 |
| Qy | 901  | CCATGTTCTCATCCCCAAGCAAAGTGCTGGGTCTGATTACTGCAACACAGAGAACGAAGA   | 960  |
| Db | 1007 | CCATGTTCTCATCCCCAAGCAAAGTGCTGGGTCTGATTACTGCAACACAGAGAACGAAGA   | 1066 |
| Qy | 961  | AGAACTTTTCCTCATACAGGATCAGCAGGGCCTCATCACACTGGGCTGGATTTCATACTCA  | 1020 |
| Db | 1067 | AGAACTTTTCCTCATACAGGATCAGCAGGGCCTCATCACACTGGGCTGGATTTCATACTCA  | 1126 |
| Qy | 1021 | CCCCACACAGACCGCGTTTCTCTCCAGTGTGACCTACACACTCACTGCTCTTACCAGAT    | 1080 |
| Db | 1127 | CCCCACACAGACCGCGTTTCTCTCCAGTGTGACCTACACACTCACTGCTCTTACCAGAT    | 1186 |
| Qy | 1081 | GATGTTGCCAGAGTCAGTAGCCATTGTTTGCTCCCCAAGTTCCAGGAAACTGGATTCTT    | 1140 |
| Db | 1187 | GATGTTGCCAGAGTCAGTAGCCATTGTTTGCTCCCCAAGTTCCAGGAAACTGGATTCTT    | 1246 |
| Qy | 1141 | TAAACTAACTGACCATGGACTAGAGGAGATTTCTTCCTGTGCGCCAGAAAGGATTTTCATCC | 1200 |
| Db | 1247 | TAAACTAACTGACCATGGACTAGAGGAGATTTCTTCCTGTGCGCCAGAAAGGATTTTCATCC | 1306 |
| Qy | 1201 | ACACAGCAAGGATCCACCTCTGTTCTGTAGCTGCAGCCACGTGACTGTTGTGGACAGAGC   | 1260 |
| Db | 1307 | ACACAGCAAGGATCCACCTCTGTTCTGTAGCTGCAGCCACGTGACTGTTGTGGACAGAGC   | 1366 |

Art Unit: 1646

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Qy      1261 AGTGACCATCACAGACCTTCGATGAGCGTTTGAGTCCAACACCTTCCAAGAACAACAAAA
1320
          |||
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1426
Qy      1321 CCATATCAGTGTACTGTAGCCCCCTTAATTTAAGCTT 1356
          |||
Db      1427 CCATATCAGTGTACTGTAGCCCCCTTAATTTAAGCTT 1462

```

In the response filed 8/22/06 Applicants argue, "Yu (AF052135) fails to disclose or suggest an hAMSH protein, let alone one having the amino acid sequence of SEQ ID NO: 1. In fact, Yu (AF052135) fails to disclose an amino acid sequence. Instead, Yu (AF052135) discloses a nucleic acid, and not a protein. Also, Yu (AF052135) fails to disclose the function of the protein as a signal transduction molecule for cell proliferation. In reply to these arguments, the Office maintained the rejection on the basis that the nucleic acid sequence in Yu (AF052135) encompasses the hAMSH protein of SEQ ID NO: 1 and the nucleotide sequence of SEQ ID NO: 2." Applicants further argue, "claim 1 is neither anticipated or rendered obvious by Yu (AF052135), because the reference fails to disclose or suggest the hAMSH protein of SEQ ID NO: 1 of claim 1. In addition, contrary to the Office's position, it is respectfully submitted that a nucleic acid sequence cannot encompass an amino acid sequence, because they are two distinct chemical entities. For this reason alone, Yu (AF052135) cannot encompass the hAMSH protein of SEQ ID NO: 1."

Applicants' arguments have been fully considered but they are not found persuasive. The protein of SEQ ID No:1 is encoded by a polynucleotide that starts with an ATG codon, the starting A nucleotide being at position 11 of SEQ ID NO:2. The polynucleotide encoding the protein of SEQ ID No:1 ends with an TGA codon, the ending A nucleotide being at position 1285 of SEQ ID NO:2. It is well known in the art that the start codon is ATG. It is also well known in the art that TGA is a stop codon.

Art Unit: 1646

Therefore when a protein is translated from a polynucleotide its translation starts at methionine (codon, ATG in DNA and AUG in mRNA) and ends at TGA (TGA in DNA and UGA in mRNA). The Color Atlas of Genetics( Eberhard Passarge), page 49, shows the codon usage in mRNA . The prediction of polypeptide sequence from exons was well known in the art as disclosed by Hutchinson and Solovyev.

It would have been prima facie obvious to a person of ordinary skill in the art at the time the invention was made to use the polynucleotide disclosed by Yu (see GenBank Accession No. AF052135 ) to determine and isolate the three fragments encoding the three possible splice variants of the protein encoded therewith using the codon identifying programs of Hutchinson and Solovyev. The ordinary artisan would have been motivated to identify the possible proteins encoded by the polynucleotide disclosed by Yu to determine the functionality encoded by the polynucleotide. A piece of DNA is useless if it cannot be associated with a function. As stated by Hutchinson (see introduction), "Improved sequence technologies and the initiatives of the Human genome project are generating large amounts of naïve DNA sequence, which has motivated the search for efficient computer algorithms to identify coding regions in genomic DNA." The ordinary artisan would have expected success at determining the polypeptides encoded by the polynucleotide disclosed by Yu (see GenBank Accession No. AF052135 ) and isolating the specific fragments of nucleic acid encoding said polypeptides because the level of skill is high in the Molecular Biology arts and polynucleotide sequences are routinely spliced, ligated, put into vectors, isolated and translated into to their encoded polypeptides. The techniques of transcription/

Art Unit: 1646

translation and polynucleotide/ protein purification are well known in the art. If more motivation is needed to look at the proteins encoded by isolated nucleic acids one has to look no further than the Human Genome Project, whose sole purpose is to provide nucleic acid sequences which will be used to determine the functionality of their encoded polypeptides.

Applicants argue that the Yu reference does not teach the DNA encodes a functional polypeptide. In response to Applicants' assertions, the discovery of a new property of a previously known compound does not make the product patentable. The function disclosed in the present claims is inherent to the protein of the prior art. Applicant asserts that Yu fails to disclose a hAMSH protein, let alone the amino acid sequence of SEQ ID NO. 1. In response to Applicant's assertion, Yu's disclosure of the nucleic acid sequence make obvious the hAMSH protein of SEQ ID NO for reason given above. Yu's cDNA clone makes obvious the nucleotide sequence of SEQ ID NO. 2 of the instant application. Applicant also asserts that Yu do not disclose the coding region for a protein. In response to Applicant's assertion, the coding region of the protein is made obvious by the nucleotide sequence even though Yu does not mention it for reasons given above.

The preceding rejection is based on the judicial precedent following *In re Fitzgerald*, 205 USPQ 594 because the prior art is silent with regard to the properties or function of the protein

***Claim Rejections - 35 USC § 102***

(a) the invention was known or used by others in this country, or patented or described in a printed publication in this or a foreign country, before the invention thereof by the applicant for a patent.

5. Claims 1, 3 and 5 are rejected under 35 U.S.C. 102(a) as being anticipated by Tanaka et al (J. Biol. Chem. 274 (27), 19129-19135, July 2, 1999 and the GenEmbl sequence Accession U73522 of the clone contained therein)

Tanaka (U73522) discloses a polynucleotide AMSH that is 100% identical to SEQ ID NO :2 (see sequence comparison below). Tanaka also discloses the isolation of a polypeptide encoded by said polynucleotide of SEQ ID NO:2 (see Fig 3). Tanaka further discloses a vector containing hAMSH (see plasmids). Therefore Tanaka meets the limitations of claims 1, 3 and 5, absent evidence to the contrary.

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: August 23, 2004, 16:45:15 ; Search time 5360 Seconds  
(without alignments)  
3428.628 Million cell updates/sec

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Perfect score: 2208  
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Art Unit: 1646

Scoring table: BLOSUM62

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Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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5: gb\_ov:\*

6: gb\_pat:\*

7: gb\_ph:\*

8: gb\_pl:\*

9: gb\_pr:\*

10: gb\_ro:\*

11: gb\_sts:\*

12: gb\_sy:\*

13: gb\_un:\*

14: gb\_vi:\*

15: em\_ba:\*

16: em\_fun:\*

17: em\_hum:\*

18: em\_in:\*

19: em\_mu:\*

20: em\_om:\*

21: em\_or:\*

22: em\_ov:\*



Art Unit: 1646

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## RESULT 3

HSU73522

LOCUS            HSU73522                      1930 bp      mRNA      linear      PRI 29-JUN-1999

DEFINITION    Homo sapiens AMSH mRNA, complete cds.

ACCESSION      U73522

VERSION        U73522.1    GI:4098123

KEYWORDS

SOURCE        Homo sapiens (human)

ORGANISM       Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE      1 (bases 1 to 1930)

AUTHORS        Tanaka,N., Kaneko,K., Asao,H., Kasai,H., Endo,Y., Fujita,T., Takeshita,T. and Sugamura,K.

TITLE           Possible involvement of a novel STAM-associated molecule 'AMSH' in intracellular signal transduction mediated by cytokines

JOURNAL        J. Biol. Chem. 274 (27), 19129-19135 (1999)

MEDLINE        99315854

PUBMED        10383417

REFERENCE      2 (bases 1 to 1930)

AUTHORS        Tanaka,N., Kaneko,K., Kasai,H., Takeshita,T. and Sugamura,K.

TITLE           Direct Submission

JOURNAL        Submitted (07-OCT-1996) Microbiology, Tohoku University School of Medicine, 2-1 Seiryomachi Aobaku, Sendai 980-77, Japan

Art Unit: 1646

FEATURES Location/Qualifiers

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ORIGIN

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| Best Local Similarity: | 100.00%   | Mismatches:   | 0    |
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US-09-831-452-1 (1-424) x HSU73522 (1-1930)

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| Db | 71  | CTGGGTAGTGCGGTAGAGGTGAATGAAGACATTCCACCCCGTCGGTACTTCCGCTCTGGA | 130 |
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| Db | 131 | GTTGAGATTATCCGAATGGCATCCATTTACTCTGAGGAAGGCAACATTGAACATGCCTTC | 190 |
| Qy | 61  | IleLeuTyrAsnLysTyrIleThrLeuPheIleGluLysLeuProLysHisArgAspTyr | 80  |
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Art Unit: 1646

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GenCore version 5.1.6

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Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%

Art Unit: 1646

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## RESULT 2

HSU73522

LOCUS            HSU73522                    1930 bp    mRNA    linear    PRI 29-JUN-1999

DEFINITION    Homo sapiens AMSH mRNA, complete cds.

ACCESSION    U73522

Art Unit: 1646

VERSION U73522.1 GI:4098123  
KEYWORDS .  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 1930)  
AUTHORS Tanaka,N., Kaneko,K., Asao,H., Kasai,H., Endo,Y., Fujita,T.,  
Takeshita,T. and Sugamura,K.  
TITLE Possible involvement of a novel STAM-associated molecule 'AMSH' in  
intracellular signal transduction mediated by cytokines  
JOURNAL J. Biol. Chem. 274 (27); 19129-19135 (1999)  
MEDLINE 99315854  
PUBMED 10383417  
REFERENCE 2 (bases 1 to 1930)  
AUTHORS Tanaka,N., Kaneko,K., Kasai,H., Takeshita,T. and Sugamura,K.  
TITLE Direct Submission  
JOURNAL Submitted (07-OCT-1996) Microbiology, Tohoku University School of  
Medicine, 2-1 Seiryomachi Aobaku, Sendai 980-77, Japan  
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ORIGIN

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Art Unit: 1646

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Art Unit: 1646

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6. The following is a quotation of the first paragraph of 35 U.S.C. 112:

The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

7. Claim 2 rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the written description requirement. The claim(s) contains subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention. The claim 2 is drawn to isolated human gene encoding the human protein hAMSH of claim 1.

The specification discloses the nucleic acid of SEQ ID NO:2, which consists of nucleotides 1-1910 encoding the polypeptide of SEQ ID NO:1. The disclosure SEQ ID NO:2 (cDNA) does not adequately describe the scope of the claimed genus of "gene", which encompasses polynucleotides comprising other undisclosed introns. A description of a genus of polynucleotides may be achieved by means of a recitation of

Art Unit: 1646

a representative number of polynucleotides, defined by the polynucleotide sequence, falling within the scope of the genus or of a recitation of structural and functional features common to members of the genus, which features constitute a substantial portion of the genus. *Regents of the University of California v. Eli Lilly & Co.*, 119 F3d 1559, 1569, 43 USPQ2d 1398, 1406 (Fed. Cir. 1997). The specification fails to provide sufficient descriptive information, such as definitive structural and functional features of the claimed genus of polynucleotide/nucleic acids. There is no description of the intron and exon structure of the claimed polynucleotide. Infact no intron structure is disclosed.

An adequate written description of a gene, requires a precise definition, such as by structure, formula and chemical name not a mere wish or plan for obtaining the claimed chemical invention. Accordingly, an adequate written description of the gene is more than a mere statement that it is part of the invention and reference to a potential method for isolating it; what is required is a description of the gene itself. Accordingly, the specification does not provide a written description of the invention of claims 2.

*Vas-Cath Inc. V. Mahurkar*, 19 USPQ2d 1111, clearly states that "applicant must convey with reasonable clarity to those skilled in the art that, as of the filing date sought, he or she was in possession of *the invention*. The invention is, for purposes of the 'written description' inquiry, *whatever is now claimed*." (See page 1117). The specification does not "clearly allow persons of ordinary skill in the art to recognize that [he or she] invented what is claimed." (See *Vas-Cath* at page 1116).

Applicant is reminded that *Vas-Cath* makes clear that the written description provision of 35 USC 112 is severable from its enablement provision (see page 115).

Art Unit: 1646

Adequate written description requires more than a mere statement that it is part of the invention and a reference to a potential method of isolating it. The nucleic acid or polypeptide is itself is required. See *Fiers v. Revel*, 25 USPQ 2d 1601 at 1606 (CAFC 1993) and *Amgen Inc. V. Chugai Pharmaceutical Co. Lts.*, 18 USPQ2d 1016.

Furthermore, In *The Reagents of the University of California v. Eli Lilly* (43 USPQ2d 1398-1412), the court held that a generic statement, which defines a genus of nucleic acids by only their functional activity, does not provide an adequate written description of the genus. The court indicated that while Applicants are not required to disclose every species encompassed by a genus, the description of a genus is achieved by the recitation of a representative number of DNA molecules, usually defined by a nucleotide sequence, falling within the scope of the claimed genus. At section B(1), the court states that "An adequate written description of a DNA...requires a precise definition, such as by structure, formula, chemical name, or physical properties', not a mere wish or plan for obtaining the claimed chemical invention".

It does not appear that Applicants were in possession of scope of the "gene" or genomic polynucleotide as claimed at the time the invention was made. There is no guidance provided to allow the skilled artisan to predict the structure of the gene other than that of SEQ ID NO:2. Even though the polynucleotide of SEQ ID NO:2 may be part of a genomic DNA segment, what besides the polynucleotide of SEQ ID NO:1 is present is not know. Due to their nature, genes are very complex structures, which are made of coding and non-coding regions (exons and introns, respectively). One skilled in the art could not predict either the number or position of introns or additional exons in

Art Unit: 1646

the claimed genomic polynucleotide or their nucleic acid sequences. Even assuming high skill of the artisan, one could not predict if there are additional coding regions in the claimed genus of variants and fragments comprising genomic DNA, beside that which is shown in SEQ ID NO:2.

With the exception of SEQ ID NO:2, the skilled artisan cannot envision the detailed chemical structure of the gene claimed and therefore conception is not achieved until reduction to practice has occurred, regardless of the complexity or simplicity of the method of isolation. Adequate written description requires more than a mere statement that it is part of the invention and reference to a potential method for isolating it. The nucleic acid itself is required. See Fiers v. Revel, 25 USPQ2d 1601, 1606 (CAFC 1993) and Amgen Inc v. Chugai Pharmaceutical Co. Ltd., 18 USPQ2d 1016.

One cannot describe what one has not achieved. See Fiddes v. Baird, 30 USPQ2d 1481, 1483. In Fiddes v. Baird, claims directed to mammalian FGFs were found unpatentable due to lack of written description for the broad class.

Therefore, only the isolated nucleic acid disclosed in SEQ ID NO:2 but not the full breadth of the claim meets the written description provision of 35 U.S.C. 112, first paragraph.

8. Claim 3 is rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the written description requirement. The claim(s) contains subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in

Art Unit: 1646

the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention. The new matter is the species of the polynucleotide which consists of the nucleotide sequence from the 11th to the 1285th nucleotide of SEQ ID No.2 . The specification does not disclose the species polynucleotide consists of the nucleotide sequence from the 11th to the 1285th nucleotide of SEQ ID No.2.

Applicant is required to cancel the new matter in the reply to this Office Action.

9. The amendment filed 12/7/05 is objected to under 35 U.S.C. 132(a) because it introduces new matter into the disclosure. 35 U.S.C. 132(a) states that no amendment shall introduce new matter into the disclosure of the invention. The added material which is not supported by the original disclosure is as follows: A polynucleotide encoding a human hAMSH, which is a signal transduction molecule for cell proliferation, wherein the polynucleotide consists of the nucleotide sequence from the 11th to the 1285th nucleotide of SEQ ID No.2. Specifically the original disclosure does not disclose the species "polynucleotide consists of the nucleotide sequence from the 11th to the 1285th nucleotide of SEQ ID No.2. "

Applicant is required to cancel the new matter in the reply to this Office Action.

***Claim Rejections - 35 USC § 101***

10. 35 U.S.C. 101 reads as follows:

Whoever invents or discovers any new and useful process, machine, manufacture, or composition of matter, or any new and useful improvement

Art Unit: 1646

thereof, may obtain a patent therefor, subject to the conditions and requirements of this title.

Claim 3 is rejected under 35 U.S.C. 101 because the claimed invention is directed to non-statutory subject matter.

Claim 3 recites a polynucleotide but do not recite that it is isolated or purified. The claim as currently recited encompasses naturally-occurring compounds. Therefore, the compounds as claimed are a product that occurs in nature and does not show the hand of man, and as such is non-statutory subject matter. It is suggested that the claims be amended to recite an "isolated and purified polynucleotide" to overcome this rejection.

11. No claims are allowed.

Art Unit: 1646

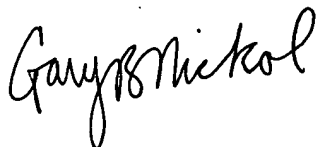
Advisory

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Nirmal S. Basi whose telephone number is 571-272-0868. The examiner can normally be reached on 9:00 AM-5:30 PM.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Gary Nickol can be reached on 571-272-0835. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see <http://pair-direct.uspto.gov>. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free). If you would like assistance from a USPTO Customer Service Representative or access to the automated information system, call 800-786-9199 (IN USA OR CANADA) or 571-272-1000.

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